

=====

Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=6; day=23; hr=8; min=41; sec=19; ms=406; ]

=====

\*\*\*\*\*

Reviewer Comments:

SEQUENCE LISTING

<110> Max-Planck-Gesellschaft zur Förderung der Wissenschaften e.V.

Please remove the foreign accent marks in the above <110> response; foreign accent marks are non-ASCII characters which cannot be processed.

<120> Cell line comprising vector encoding truncated FLK-1 receptor  
Div. of US 09/766 678 (Pat. No. 6 872 699)

Please remove "Div. of US 09/766 678 (Pat. No. 6 872 699)" from the above <120> response; just show the invention title. Move all prior application data to the <150> and the <151> lines. See below:

<150> US 09/766,678

<151> 2001-01-23

The <150> is the prior application number; the <151> is the prior filing date.

<210> 1

<211> 5470

<212> DNA

<213> Unknown

<220>

<223> SEQ ID NO: 1

The above <223> response is an insufficient explanation of "<213>

Unknown": although the <213> response is "Unknown", please try to indicate the source of the genetic material. Same type of error in Sequences 2-11.

\*\*\*\*\*

Application No: 10799782 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2009-06-15 15:22:43.641  
**Finished:** 2009-06-15 15:22:45.942  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 301 ms  
**Total Warnings:** 11  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 11  
**Actual SeqID Count:** 11

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)

<210> 1  
 <211> 5470  
 <212> DNA  
 <213> Unknown

<220>  
 <223> SEQ ID NO: 1

<220>  
 <221> CDS  
 <222> (286)...(4386)

<400> 1  
 tatagggcga attgggtacg ggaccccccct cgaggtcgac ggtatcgata agcttgatat 60  
 cgaattcggg cccagactgt gtcccgccagc cgggataacc tggctgaccc gattccgcgg 120  
 acaccgctga cagccgcggc tggagccagg gcccgggtgc cccgcgtct ccccggtctt 180  
 gcgcgtgcggg ggccataccg cctctgtac ttcttcgcgg gccaggacg gagaaggagt 240  
 ctgtgcctga gaaactgggc tctgtgccc ggcgcgaggt gcagg atg gag agc aag 297  
 Met Glu Ser Lys  
 1

gcg ctg cta gct gtc gct ctg tgg ttc tgc gtg gag acc cga gcc gcc 345  
 Ala Leu Ala Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala Ala  
 5 10 15 20

tct gtg ggt ttg act ggc gat ttt ctc cat ccc ccc aag ctc agc aca 393  
 Ser Val Gly Leu Thr Gly Asp Phe Leu His Pro Pro Lys Leu Ser Thr  
 25 30 35

cag aaa gac ata ctg aca att ttg gca aat aca acc ctt cag att act 441  
 Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile Thr  
 40 45 50

tgc agg gga cag cgg gac ctg gac tgg ctt tgg ccc aat gct cag cgt 489  
 Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln Arg  
 55 60 65

gat tct gag gaa agg gta ttg gtg act gaa tgc ggc ggt ggt gac agt 537  
 Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly Gly Asp Ser  
 70 75 80

atc ttc tgc aaa aca ctc acc att ccc agg gtg gtt gga aat gat act 585  
 Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp Thr  
 85 90 95 100

gga gcc tac aag tgc tcg tac cgg gac gtc gac ata gcc tcc act gtt 633  
 Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr Val  
 105 110 115

tat gtc tat gtt cga gat tac aga tca cca ttc atc gcc tct gtc agt 681  
 Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser  
 120 125 130

gac cag cat ggc atc gtg tac atc acc gag aac aag aac aaa act gtg		729
Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr Val		
135	140	145
gtg atc ccc tgc cga ggg tcg att tca aac ctc aat gtg tct ctt tgc		777
Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu Cys		
150	155	160
gct agg tat cca gaa aag aga ttt gtt ccg gat gga aac aga att tcc		825
Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser		
165	170	175
180		
tgg gac agc gag ata ggc ttt act ctc ccc agt tac atg atc agc tat		873
Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr Met Ile Ser Tyr		
185	190	195
gcc ggc atg gtc ttc tgt gag gca aag atc aat gat gaa acc tat cag		921
Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Thr Tyr Gln		
200	205	210
tct atc atg tac ata gtt gtg gtt gta gga tat agg att tat gat gtg		969
Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr Asp Val		
215	220	225
att ctg agc ccc ccg cat gaa att gag cta tct gcc gga gaa aaa ctt		1017
Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala Gly Glu Lys Leu		
230	235	240
gtc tta aat tgt aca gcg aga aca gag ctc aat gtg ggg ctt gat ttc		1065
Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Leu Asp Phe		
245	250	255
260		
acc tgg cac tct cca cct tca aag tct cat cat aag aag att gta aac		1113
Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys Lys Ile Val Asn		
265	270	275
cgg gat gtg aaa ccc ttt cct ggg act gtg gcg aag atg ttt ttg agc		1161
Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys Met Phe Leu Ser		
280	285	290
acc ttg aca ata gaa agt gtg acc aag agt gac caa ggg gaa tac acc		1209
Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln Gly Glu Tyr Thr		
295	300	305
tgt gta gcg tcc agt gga cgg atg atc aag aga aat aga aca aca ttt gtc		1257
Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn Arg Thr Phe Val		
310	315	320
cga gtt cac aca aag cct ttt att gct ttc ggt agt ggg atg aaa tct		1305
Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser Gly Met Lys Ser		
325	330	335
340		
ttg gtg gaa gcc aca gtg ggc agt caa gtc cga atc cct gtg aag tat		1353
Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile Pro Val Lys Tyr		
345	350	355

ctc agt tac cca gct cct gat atc aaa tgg tac aga aat gga agg ccc Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg Asn Gly Arg Pro 360	365	370	1401	
att gag tcc aac tac aca atg att gtt ggc gat gaa ctc acc atc atg Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu Leu Thr Ile Met 375	380	385	1449	
gaa gtg act gaa aga gat gca gga aac tac acg gtc atc ctc acc aac Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val Ile Leu Thr Asn 390	395	400	1497	
ccc att tca atg gag aaa cag agc cac atg gtc tct ctg gtt gtg aat Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser Leu Val Val Asn 405	410	415	420	1545
gtc cca ccc cag atc ggt gag aaa gcc ttg atc tcg cct atg gat tcc Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser Pro Met Asp Ser 425	430	435	1593	
tac cag tat ggg acc atg cag aca ttg aca tgc aca gtc tac gcc aac Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr Val Tyr Ala Asn 440	445	450	1641	
cct ccc ctg cac cac atc cag tgg tac tgg cag cta gaa gaa gcc tgc Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu Glu Glu Ala Cys 455	460	465	1689	
tcc tac aga ccc ggc caa aca agc ccg tat gct tgt aaa gaa tgg aga Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys Lys Glu Trp Arg 470	475	480	1737	
cac gtg gag gat ttc cag ggg gga aac aag atc gaa gtc acc aaa aac His Val Glu Asp Phe Gln Gly Asn Lys Ile Glu Val Thr Lys Asn 485	490	495	500	1785
caa tat gcc ctg att gaa gga aaa aac aaa act gta agt acg ctg gtc Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val Ser Thr Leu Val 505	510	515	1833	
atc caa gct gcc aac gtg tca gcg ttg tac aaa tgt gaa gcc atc aac Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys Glu Ala Ile Asn 520	525	530	1881	
aaa gcg gga cga gga gag agg gtc atc tcc ttc cat gtg atc agg ggt Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His Val Ile Arg Gly 535	540	545	1929	
cct gaa att act gtg caa cct gct gcc cag cca act gag cag gag agt Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr Glu Gln Glu Ser 550	555	560	1977	
gtg tcc ctg ttg tgc act gca gac aga aat acg ttt gag aac ctc acg Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe Glu Asn Leu Thr 565	570	575	580	2025
tgg tac aag ctt ggc tca cag gca aca tcg gtc cac atg ggc gaa tca			2073	

Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His Met Gly Glu Ser			
585	590	595	
ctc aca cca gtt tgc aag aac ttg gat gct ctt tgg aaa ctg aat ggc			2121
Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp Lys Leu Asn Gly			
600	605	610	
acc atg ttt tct aac agc aca aat gac atc ttg att gtg gca ttt cag			2169
Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile Val Ala Phe Gln			
615	620	625	
aat gcc tct ctg cag gac caa ggc gac tat gtt tgc tct gct caa gat			2217
Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys Ser Ala Gln Asp			
630	635	640	
aag aag acc aag aaa aga cat tgc ctg gtc aaa cag ctc atc atc cta			2265
Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln Leu Ile Ile Leu			
645	650	655	660
gag cgc atg gca ccc atg atc acc gga aat ctg gag aat cag aca aca			2313
Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu Asn Gln Thr Thr			
665	670	675	
acc att ggc gag acc att gaa gtg act tgc cca gca tct gga aat cct			2361
Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala Ser Gly Asn Pro			
680	685	690	
acc cca cac att aca tgg ttc aaa gac aac gag acc ctg gta gaa gat			2409
Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr Leu Val Glu Asp			
695	700	705	
tca ggc att gta ctg aga gat ggg aac cgg aac ctg act atc cgc agg			2457
Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu Thr Ile Arg Arg			
710	715	720	
gtg agg aag gag gat gga ggc ctc tac acc tgc cag gcc tgc aat gtc			2505
Val Arg Lys Glu Asp Gly Leu Tyr Thr Cys Gln Ala Cys Asn Val			
725	730	735	740
ctt ggc tgt gca aga gcg gag acg ctc ttc ata ata gaa ggt gcc cag			2553
Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile Glu Gly Ala Gln			
745	750	755	
gaa aag acc aac ttg gaa gtc att atc ctc gtc ggc act gca gtg att			2601
Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly Thr Ala Val Ile			
760	765	770	
gcc atg ttc ttc tgg ctc ctt ctt gtc att gtc cta cgg acc gtt aag			2649
Ala Met Phe Phe Trp Leu Leu Val Ile Val Leu Arg Thr Val Lys			
775	780	785	
cgg gcc aat gaa ggg gaa ctg aag aca ggc tac ttg tct att gtc atg			2697
Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val Met			
790	795	800	
gat cca gat gaa ttg ccc ttg gat gag cgc tgt gaa cgc ttg cct tat			2745
Asp Pro Asp Glu Leu Pro Leu Asp Glu Arg Cys Glu Arg Leu Pro Tyr			

805	810	815	820	
gat gcc agc aag tgg gaa ttc ccc agg gac cg <sup>g</sup> ctg aaa cta gga aaa Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp Arg Leu Lys Leu Gly Lys				2793
825	830	835		
cct ctt ggc cgc ggt gcc ttc ggc caa gtg att gag gca gac gct ttt Pro Leu Gly Arg Gly Ala Phe Gly Gln Val Ile Glu Ala Asp Ala Phe				2841
840	845	850		
gga att gac aag aca gcg act tgc aaa aca gta gcc gtc aag atg ttg Gly Ile Asp Lys Thr Ala Thr Cys Lys Thr Val Ala Val Lys Met Leu				2889
855	860	865		
aaa gaa gga gca aca cac agc gag cat cga gcc ctc atg tct gaa ctc Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu Met Ser Glu Leu				2937
870	875	880		
aag atc ctc atc cac att ggt cac cat ctc aat gtg gtg aac ctc cta Lys Ile Leu Ile His Ile Gly His His Leu Asn Val Val Asn Leu Leu				2985
885	890	895	900	
ggc gcc tgc acc aag ccg gga ggg cct ctc atg gtg att gtg gaa ttc Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu Phe				3033
905	910	915		
tgc aag ttt gga aac cta tca act tac tta cgg ggc aag aga aat gaa Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Gly Lys Arg Asn Glu				3081
920	925	930		
ttt gtt ccc tat aag agc aaa ggg gca cgc ttc cgc cag ggc aag gac Phe Val Pro Tyr Lys Ser Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp				3129
935	940	945		
tac gtt ggg gag ctc tcc gtg gat ctg aaa aga cgc ttg gac agc atc Tyr Val Gly Glu Leu Ser Val Asp Leu Lys Arg Arg Leu Asp Ser Ile				3177
950	955	960		
acc agc agc cag agc tct gcc agc tca ggc ttt gtt gag gag aaa tcg Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser				3225
965	970	975	980	
ctc agt gat gta gag gaa gaa gaa gct tct gaa gaa ctg tac aag gac Leu Ser Asp Val Glu Glu Glu Ala Ser Glu Glu Leu Tyr Lys Asp				3273
985	990	995		
ttc ctg acc ttg gag cat ctc atc tgt tac agc ttc caa gtg gct Phe Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala				3318
1000	1005	1010		
aag ggc atg gag ttc ttg gca tca agg aag tgt atc cac agg gac Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp				3363
1015	1020	1025		
ctg gca gca cga aac att ctc cta tcg gag aag aat gtg gtt aag Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn Val Val Lys				3408
1030	1035	1040		

atc tgt gac ttc ggc ttg gcc cg	gac att tat aaa gac ccg gat	3453
Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp		
1045 1050 1055		
tat gtc aga aaa gga gat gcc cga ctc cct ttg aag tgg atg gcc	3498	
Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met Ala		
1060 1065 1070		
ccg gaa acc att ttt gac aga gta tac aca att cag agc gat gtg	3543	
Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val		
1075 1080 1085		
tgg tct ttc ggt gtg ttg ctc tgg gaa ata ttt tcc tta ggt gcc	3588	
Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala		
1090 1095 1100		
tcc cca tac cct ggg gtc aag att gat gaa gaa ttt tgt agg aga	3633	
Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe Cys Arg Arg		
1105 1110 1115		
ttg aaa gaa gga act aga atg cg gct cct gac tac act acc cca	3678	
Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro		
1120 1125 1130		
gaa atg tac cag acc atg ctg gac tgc tgg cat gag gac ccc aac	3723	
Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Glu Asp Pro Asn		
1135 1140 1145		
cag aga ccc tcg ttt tca gag ttg gtg gag cat ttg gga aac ctc	3768	
Gln Arg Pro Ser Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu		
1150 1155 1160		
ctg caa gca aat gcg cag cag gat ggc aaa gac tat att gtt ctt	3813	
Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys Asp Tyr Ile Val Leu		
1165 1170 1175		
cca atg tca gag aca ctg agc atg gaa gag gat tct gga ctc tcc	3858	
Pro Met Ser Glu Thr Leu Ser Met Glu Glu Asp Ser Gly Leu Ser		
1180		